

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/577,601
Source: IFWP
Date Processed by STIC: 05/11/2006

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IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/577,601

DATE: 05/11/2006
TIME: 11:12:42

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05112006\J577601.raw

3 <110> APPLICANT: KANEKA CORPORATION
 5 <120> TITLE OF INVENTION: NOVEL ACETOACETYL-CoA REDUCTASE AND PROCESS FOR PRODUCING
 OPTICALLY
 6 ACTIVE ALCOHOL
 8 <130> FILE REFERENCE: B030435W001
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/577,601
 C--> 10 <141> CURRENT FILING DATE: 2006-04-27
 10 <150> PRIOR APPLICATION NUMBER: JP2003-380987
 11 <151> PRIOR FILING DATE: 2003-11-11
 13 <160> NUMBER OF SEQ ID NOS: 15
 15 <170> SOFTWARE: PatentIn version 3.1
 17 <210> SEQ ID NO: 1
 18 <211> LENGTH: 245
 19 <212> TYPE: PRT
 20 <213> ORGANISM: Achromobacter xylosoxidans subsp. denitrificans
 22 <400> SEQUENCE: 1
 23 Met Ser Gly Leu Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
 24 1 5 10 15
 26 Thr Ser Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
 27 20 25 30
 29 Gly Cys Gly Pro Ser Arg Asn Tyr Gln Gln Trp Leu Asp Glu Gln Ala
 30 35 40 45
 32 Ala Gln Gly Tyr Thr Phe Tyr Ala Ser Val Gly Asn Val Ser Asp Trp
 33 50 55 60
 35 Glu Ser Thr Val Glu Ala Phe Glu Arg Val Lys Arg Asp Met Gly Pro
 36 65 70 75 80
 38 Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Gly Leu Phe
 39 85 90 95
 41 Arg Lys Met Ser Ala Asp Asp Trp Arg Ala Val Ile Asp Thr Asn Leu
 42 100 105 110
 44 Asn Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Asp Met Val Glu
 45 115 120 125
 47 Arg Gln Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln Lys
 48 130 135 140
 50 Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Ile His
 51 145 150 155 160
 53 Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Ser Lys Gly Ile Thr
 54 165 170 175
 56 Val Asn Thr Val Ser Pro Gly Tyr Ile Gly Thr Asp Met Val Arg Ala
 57 180 185 190
 59 Ile Arg Pro Asp Val Leu Glu Lys Ile Val Ala Thr Ile Pro Val Arg
 60 195 200 205
 62 Arg Leu Gly Thr Pro Glu Glu Ile Ala Ser Ile Thr Ser Trp Leu Ala
 63 210 215 220

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65 Ser Asp Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn Gly
66 225 230 235 240
68 Gly Leu His Met Gly
69 245
72 <210> SEQ ID NO: 2
73 <211> LENGTH: 738
74 <212> TYPE: DNA
75 <213> ORGANISM: Achromobacter xylosoxidans subsp. denitrificans
77 <220> FEATURE:
78 <221> NAME/KEY: CDS
79 <222> LOCATION: (1)..(738)
81 <400> SEQUENCE: 2
82 atg agc gga aaa ctg gct tac aca ggc ggg atg ggc ggt atc ggc 48
83 Met Ser Gly Lys Leu Ala Tyr Val Thr Gly Gly Met Gly Ile Gly
84 1 5 10 15
86 acc tca att tgc cag cgc ctg gcc aaa gat ggc ttt cgc gtg gtg gca 96
87 Thr Ser Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
88 20 25 30
90 ggc tgc ggc ccc agc cgc aat tac cag caa tgg ctg gat gaa cag gcg 144
91 Gly Cys Gly Pro Ser Arg Asn Tyr Gln Gln Trp Leu Asp Glu Gln Ala
92 35 40 45
94 gcg cag ggc tat acg ttc tac gcg tca gtg ggc aac gtg tcc gat tgg 192
95 Ala Gln Gly Tyr Thr Phe Tyr Ala Ser Val Gly Asn Val Ser Asp Trp
96 50 55 60
98 gag tcc acg gta gaa gca ttc gag cgc gtc aag cgg gac atg ggc ccg 240
99 Glu Ser Thr Val Glu Ala Phe Glu Arg Val Lys Arg Asp Met Gly Pro
100 65 70 75 80
102 gtc gat gtg ctg gtc aac aac gcg ggc atc acc cgc gac ggc ctg ttc 288
103 Val Asp Val Leu Val Asn Asn Ala Gly Ile Thr Arg Asp Gly Leu Phe
104 85 90 95
106 cgc aag atg agc gcc gac gac tgg cgc gcg gtc atc gac acc aac ctg 336
107 Arg Lys Met Ser Ala Asp Asp Trp Arg Ala Val Ile Asp Thr Asn Leu
108 100 105 110
110 aac agc ctc ttc aac gtg acc aag cag gtg atc gac gac atg gtc gag 384
111 Asn Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Asp Met Val Glu
112 115 120 125
114 cgc cag tgg ggc cgc atc gtc aac atc agc tcg gtg aac ggg cag aag 432
115 Arg Gln Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln Lys
116 130 135 140
118 ggg cag ttc ggc cag acg aac tat tcc acg gcg aag gcg ggc atc cat 480
119 Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Ile His
120 145 150 155 160
122 ggc ttc acc atg gcg ctg gcg cag gaa gtg ggc agc aag ggc atc acg 528
123 Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Ser Lys Gly Ile Thr
124 165 170 175
126 gtc aac acg gtg tcg ccg ggc tac atc ggc acg gac atg gtt cgc gcc 576
127 Val Asn Thr Val Ser Pro Gly Tyr Ile Gly Thr Asp Met Val Arg Ala
128 180 185 190
130 atc cgt ccg gac gtg ctg gaa aag atc gtc gcc acc att ccg gtg cgc 624

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131 Ile Arg Pro Asp Val Leu Glu Lys Ile Val Ala Thr Ile Pro Val Arg
132      195          200          205
134 cgc ctg ggc acg ccg gag gaa atc gcg tcc atc acg tcg tgg ctg gcc      672
135 Arg Leu Gly Thr Pro Glu Glu Ile Ala Ser Ile Thr Ser Trp Leu Ala
136      210          215          220
138 tcg gat gag tct ggg ttt tcg acg ggc gcg gac ttc tcg ctc aac ggc      720
139 Ser Asp Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn Gly
140 225          230          235          240
142 ggc ctg cat atg ggc tga
143 Gly Leu His Met Gly
144      245
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 246
149 <212> TYPE: PRT
150 <213> ORGANISM: Ralstonia eutropha
152 <400> SEQUENCE: 3
153 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
154 1          5          10          15
156 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
157      20          25          30
159 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
160      35          40          45
162 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
163      50          55          60
165 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
166 65          70          75          80
168 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
169      85          90          95
171 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
172      100         105         110
174 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
175      115         120         125
177 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
178      130         135         140
180 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
181 145         150         155         160
183 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
184      165         170         175
186 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
187      180         185         190
189 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
190      195         200         205
192 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
193      210         215         220
195 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
196 225         230         235         240
198 Gly Gly Leu His Met Gly
199      245
202 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING DATE: 05/11/2006
 PATENT APPLICATION: US/10/577,601 TIME: 11:12:42

Input Set : A:\PTO.RJ.txt
 Output Set: N:\CRF4\05112006\J577601.raw

203 <211> LENGTH: 741		
204 <212> TYPE: DNA		
205 <213> ORGANISM: Ralstonia eutropha		
207 <220> FEATURE:		
208 <221> NAME/KEY: CDS		
209 <222> LOCATION: (1)..(741)		
211 <400> SEQUENCE: 4		
212 atg act cag cgc att gcg tat gtg acc ggc ggc atg ggt ggt atc gga	48	
213 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly		
214 1 5 10 15		
216 acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt gtg gtg gcc	96	
217 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala		
218 20 25 30		
220 ggt tgc ggc ccc aac tcg ccg cgc gaa aag tgg ctg gag cag cag	144	
221 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln		
222 35 40 45		
224 aag gcc ctg ggc ttc gat ttc att gcc tcg gaa ggc aat gtc gct gac	192	
225 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp		
226 50 55 60		
228 tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc gag gtc ggc	240	
229 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly		
230 65 70 75 80		
232 gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc gac gtg gtg	288	
233 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val		
234 85 90 95		
236 ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac	336	
237 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn		
238 100 105 110		
240 ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac ggc atg gcc	384	
241 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala		
242 115 120 125		
244 gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg aac ggg cag	432	
245 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln		
246 130 135 140		
248 aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag gcc ggc ctg	480	
249 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu		
250 145 150 155 160		
252 cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc aag ggc gtg	528	
253 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val		
254 165 170 175		
256 acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac atg gtc aag	576	
257 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys		
258 180 185 190		
260 gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg atc ccg gtc	624	
261 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val		
262 195 200 205		
264 aag cgc ctg ggc ctg ccg gaa gag atc gcc tcg atc tgc gcc tgg ttg	672	
265 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu		
266 210 215 220		

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268 tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc tcg ctc aac	720
269 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn	
270 225 230 235 240	
272 ggc ggc ctg cat atg ggc tga	741
273 Gly Gly Leu His Met Gly	
274 245	
277 <210> SEQ ID NO: 5	
278 <211> LENGTH: 19	
279 <212> TYPE: DNA	
280 <213> ORGANISM: Artificial Sequence	
282 <220> FEATURE:	
283 <223> OTHER INFORMATION: Primer 1	
285 <220> FEATURE:	
286 <221> NAME/KEY: misc_feature	
287 <222> LOCATION: (6)..(6)	
288 <223> OTHER INFORMATION: n represents a, t, g or c	
290 <220> FEATURE:	
291 <221> NAME/KEY: misc_feature	
292 <222> LOCATION: (12)..(12)	
293 <223> OTHER INFORMATION: n represents a, t, g or c	
295 <400> SEQUENCE: 5	
W--> 296 caggntaya cnttytayg	19
299 <210> SEQ ID NO: 6	
300 <211> LENGTH: 20	
301 <212> TYPE: DNA	
302 <213> ORGANISM: Artificial Sequence	
304 <220> FEATURE:	
305 <223> OTHER INFORMATION: Primer 2	
307 <220> FEATURE:	
308 <221> NAME/KEY: misc_feature	
309 <222> LOCATION: (12)..(12)	
310 <223> OTHER INFORMATION: n represents a, t, g or c	
312 <220> FEATURE:	
313 <221> NAME/KEY: misc_feature	
314 <222> LOCATION: (15)..(15)	
315 <223> OTHER INFORMATION: n represents a, t, g or c	
317 <400> SEQUENCE: 6	
W--> 318 gcdatytcyt cnggngtaycc	20
321 <210> SEQ ID NO: 7	
322 <211> LENGTH: 25	
323 <212> TYPE: DNA	
324 <213> ORGANISM: Artificial Sequence	
326 <220> FEATURE:	
327 <223> OTHER INFORMATION: Primer 3	
329 <400> SEQUENCE: 7	
330 cgtcggcgct catcttgcgg aacag	25
333 <210> SEQ ID NO: 8	
334 <211> LENGTH: 25	
335 <212> TYPE: DNA	

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/11/2006
PATENT APPLICATION: US/10/577,601 TIME: 11:12:43

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05112006\J577601.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 6,12
Seq#:6; N Pos. 11,15

VERIFICATION SUMMARY DATE: 05/11/2006
PATENT APPLICATION: US/10/577,601 TIME: 11:12:43

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\05112006\J577601.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:296 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0